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Year: 2018

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DOI: <https://doi.org/10.1038/mi.2017.74>

Posted at the Zurich Open Repository and Archive, University of Zurich

ZORA URL: <https://doi.org/10.5167/uzh-167357>

Journal Article

Published Version



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Originally published at:

Schwerd, T; Bryant, R V; Pandey, S; Capitani, M; Meran, L; Cazier, J-B; Jung, J; Mondal, K; Parkes, M; Mathew, C G; Fiedler, K; McCarthy, D J; WGS500 Consortium; Oxford IBD cohort study investigators; COLORS in IBD group investigators; UK IBD Genetics Consortium; Sullivan, P B; Rodrigues, A; Travis,

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# NOX1 loss-of-function genetic variants in patients with inflammatory bowel disease

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Genetic defects that affect intestinal epithelial barrier function can present with very early-onset inflammatory bowel disease (VEOIBD). Using whole-genome sequencing, a novel hemizygous defect in *NOX1* encoding NADPH oxidase 1 was identified in a patient with ulcerative colitis-like VEOIBD. Exome screening of 1,878 pediatric patients identified further seven male inflammatory bowel disease (IBD) patients with rare *NOX1* mutations. Loss-of-function was validated in p.N122H and p.T497A, and to a lesser degree in p.Y470H, p.R287Q, p.I67M, p.Q293R as well as the previously described p.P330S, and the common *NOX1* SNP p.D360N (rs34688635) variant. The missense mutation p.N122H abrogated reactive oxygen species (ROS) production in cell lines, *ex vivo* colonic explants, and patient-derived colonic organoid cultures. Within colonic crypts, *NOX1* constitutively generates a high level of ROS in the crypt lumen. Analysis of 9,513 controls and 11,140 IBD patients of non-Jewish European ancestry did not reveal an association between p.D360N and IBD. Our data suggest that loss-of-function variants in *NOX1* do not cause a Mendelian disorder of high penetrance but are a context-specific modifier. Our results implicate that variants in *NOX1* change brush border ROS within colonic crypts at the interface between the epithelium and luminal microbes.

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Received 12 May 2017; accepted 20 July 2017; published online 1 November 2017. doi:10.1038/mi.2017.74

## INTRODUCTION

In the gastrointestinal (GI) tract, the epithelium is the primary barrier separating the high density of microbes in the intestinal lumen from the immune cells in the lamina propria. Defects in epithelial barrier function predispose to inflammatory bowel disease (IBD) in humans and cause intestinal inflammation in animal models.<sup>1,2</sup>

Genetic risk variants for IBD in loci linked to genes relevant for epithelial integrity have been identified by genome-wide association studies (e.g., *GNA12*, *HNF4A*, *MUC19*, or *XPB1*).<sup>3,4</sup> In addition, there is an expanding group of monogenic defects associated with significant functional impact on intestinal epithelial barrier function.<sup>5,6</sup> Defects in intestinal epithelial guanylylase gene *GUCY2C* or the solute carrier family 9 member 3 (*SLC9A3*) encoding the sodium hydrogen exchanger NHE3 cause congenital diarrhea and Crohn's disease-like intestinal inflammation in ~30% of cases.<sup>7,8</sup> Likewise, defects in *IKBKG* causing impaired nuclear factor- $\kappa$ B signaling result in epithelial apoptosis and intestinal inflammation.<sup>9</sup> In patients with *TTC7A* deficiency, defects in epithelial PI4K and Rho signaling cause disturbed epithelial polarization leading to multiple intestinal atresia or very early-onset intestinal inflammation.<sup>10–12</sup>

Recently, we reported a common *NOX1* missense mutation associated with ulcerative colitis (UC) in males of Ashkenazi Jewish ancestry, in addition to a rare *NOX1* mutation in a patient with early onset of intestinal inflammation.<sup>13</sup> *NOX1* is the catalytic subunit of superoxide-generating nicotinamide adenine dinucleotide phosphate (NADPH) oxidase complex 1, and is comprised of *NOX1*, *p22<sup>phox</sup>*, *NOXA1*, *NOXO1*, and *Rac1-GTP*.<sup>14–16</sup> *NOX1* is a close structural homolog of *NOX2*, the catalytic subunit of the multimeric NADPH oxidase complex 2 (*NOX2*, *p22<sup>phox</sup>*, *p67<sup>phox</sup>*, *p47<sup>phox</sup>*, *p40<sup>phox</sup>*, and *Rac2-GTP*), the enzyme responsible for the microbicidal “respiratory burst” in phagocytes. However, in contrast to *NOX2*, *NOX1* is located in the membrane of the intestinal epithelial cells<sup>17–21</sup> and, may have additional functions in endothelial cells and in non-GI epithelium.<sup>22</sup>

Here we investigate several loss-of-function missense variants in *NOX1* that were identified by whole-genome and whole-exome sequencing in patients with very early-onset IBD (VEOIBD). We identified eight males with six hemizygous non-synonymous *NOX1* variants, with variable functional impact upon reactive oxygen species (ROS) production as compared to the previously described p.P330S and the common p.D360N (rs34688635) variants. We identified two variants with nearly complete loss of function and a further four variants with reduced activity. Primary patient-derived intestinal colonic organoids of the loss-of-function variant p.N122H were used to validate those findings.

## RESULTS

### Index patient

We studied a male patient of Caucasian origin who presented with bloody stools and failure to thrive at the age of 2 years

(Table 1). He was diagnosed with IBD at the age of 5 years. His disease progressed from proctitis to pancolitis at the age of 8 years without upper GI involvement (Figure 1a). Histological examination of colonic specimens showed crypt architectural distortion, cryptitis, and crypt abscess formation (Figure 1a). Histologic assessment of epithelial cell proliferation or goblet cell formation did not reveal marked differences compared to inflammatory controls (Supplementary Figure S1 online). The patient required oral corticosteroid therapy at diagnosis, followed by thiopurine and then methotrexate therapy. After years of poorly controlled inflammation, mucosal healing was achieved with anti-tumor necrosis factor therapy (adalimumab). Nine years after diagnosis, his disease was complicated by Epstein–Barr virus-associated hemophagocytic lymphohistiocytosis whilst on azathioprine therapy, requiring intensive care therapy. Mutations in *XIAP* and *SAP* were excluded at that time. There was no family history of IBD.

Whole-genome sequencing of the patient led to the identification of a novel hemizygous variant in the NADPH oxidase 1 *NOX1*; NM\_007052; c.A364C; p.N122H (Supplementary Figure S2). The mutation was validated with Sanger sequencing and inherited in an X-linked manner from the patient's mother (Figure 1b). The mutation is not present in 1,678 Crohn's disease (CD), 1,089 UC patients, or 1,862 non-IBD controls, or in any public exome database covering an excess of 120,000 human alleles (e.g., 1000 Genomes and Exome Aggregation Consortium (ExAC)), thus supporting the view that this is an extremely rare genetic variant (Supplementary Table 1). The amino acid N122 is located in the third transmembrane domain and is evolutionary highly conserved across species (Figure 1c). *In silico* analysis by several tools, including SIFT, PolyPhen-2, and CADD,<sup>23</sup> predicted that the mutation causes a loss-of-function (Supplementary Table 2). Furthermore, the p.N122H variant affects all known isoforms of *NOX1* (Figure 1d). Other hemizygous, homozygous, or compound heterozygous variants in the index patient were considered unlikely pathogenic (Supplementary Table 3). None of these variants have been described as causative for IBD or Epstein–Barr virus-induced hemophagocytosis.

### NOX1 expression and epithelial-derived ROS

To understand the relative distribution of ROS-generating NADPH oxidases in the human GI tract and to compare non-inflamed homeostasis with inflammatory conditions, we determined the mRNA expression pattern of several NADPH oxidases and their subunits. Consistent with previous literature,<sup>17–20</sup> *NOX1* is highly expressed in the colonic epithelium with a gradient from ileum to the distal colon (Figure 1e). The subunits *NOXA1* and *NOXO1* are constitutively expressed along the human GI tract (Figure 1e). Whereas phagocytic *NOX2* can be detected even in the non-inflamed mucosa, we observed no expression of *NOX4* and very low expression of *NOX5* (Supplementary Figure S3a). In parallel with the *NOX1* expression gradient, we found increased ROS generation in

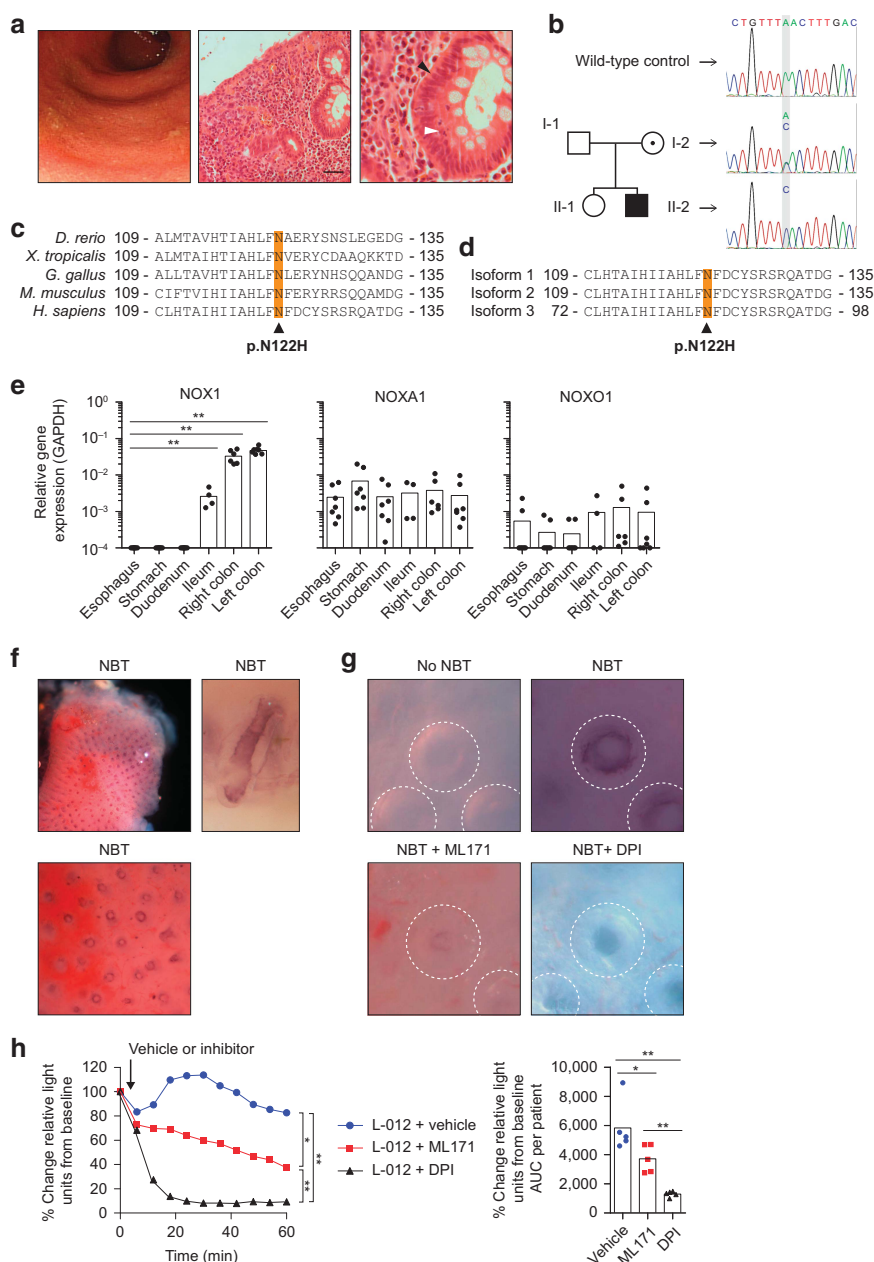
**Table 1 Clinical characterization of male patients with non-synonymous NOX1 hemizygous variants**

Patient ID	NOX1 variants	Gender	Age of diagnosis (of symptoms) in years	Diagnosis Paris class. <sup>62</sup>	Family history for IBD	Intestinal and extra-intestinal symptoms/findings on examination (age in years)	Histology	Treatment for IBD
P1	c.A364C p.N122H	M	5 (2)	IBDU; E4	Negative	Presented with bloody stools and failure to thrive (2), progression from proctitis (5) to pancolitis (19), terminal ileum normal, perianal skin tags, EBV-associated HLH (14) whilst on AZA	Cryptitis, crypt architectural distortion, crypt abscesses, focal Paneth cell metaplasia, single micro-granuloma	Oral CS, ASA, AZA, MTX, ADA
P2	c.T1408C p.Y470H	M	9.7	CD; L3L4a, B1	Negative	Initially presented with weight loss and rectal bleeding	Granulomata, neutrophilic infiltration into crypts and surface epithelium	Oral CS, IFX, MTX
P3	c.C201G p.I67M	M	8.6 (7.8)	UC; E4	Mother (UC)	Presented with abdominal pain and alternating formed stool/diarrhea with blood/mucous (7.8). At diagnosis microscopic pancolitis (8.6), later macroscopic disease in rectosigmoid (17.5), no EIMs	Neutrophil infiltrate, (peri-) cryptitis, branching, and focal dropout of glands, regeneration. No granuloma	5-ASA
P4	c.G860A p.R287Q	M	9.9 (9.5)	CD; L3L4a, B1p	Brother and aunt (CD)	Presented with abdominal pain and loose stools (9.9), right colon and ileal disease distribution (13), perianal skin tags and fistula (15.8)	Granulomata, focal branching, (peri-) cryptitis, intraepithelial lymphocytes, lymphoplasmacytic infiltrate, basal cell hyperplasia	5-ASA, SALZ, AB
P5	c.G860A p.R287Q	M	10.5 (8.5)	CD; L3L4ab; B2p	Brother and aunt (CD)	Presented with long-standing abdominal pain, variably loose stools/constipation (8.5), and more recent periodic blood PR (10.3). Diagnostic scope primarily small bowel disease and minor colonic involvement; perianal fistula (10.5)	Cryptitis, pericryptitis, crypt distortion, cell infiltrate, giant cells. No granulomas	5-ASA, AB, IFX, CS, NUT, ADA. Ileocecal resection for stricture (12.8), second ileocecal resection (15.6)
P6	c.G860A p.R287Q	M	5.7 (5.3)	UC; E2	Cousins (CD or UC)	Presented with rectal bleeding (5.3). At scope, diagnosed with left sided colitis (5.7). No GI Sx since age 9 years old. At 15 years old, diagnosed with stage IVB non-bulk nodular sclerosing Hodgkin's disease. In remission following therapy	Chronic inflammatory infiltrate	Previously SALZ. Currently on no therapy
P7	c. A878G p.Q293R	M	9.7 (9.4)	CD; L2L4a	Negative	Presented with bloody diarrhea, arthralgia, lethargy, and weight loss (9.4). Pancolitis at diagnosis (9.7), upper GI inflammation (17.5), arthralgias	Cryptitis, crypt abscesses, Paneth cell metaplasia, apoptotic epithelial cells involving most colonic crypts, transepithelial inflammation, No granulomas.	AB, IV and oral CS, SALZ, MTX, IFX
P8	c.A1489G p.T497A	M	7.1 (7.0)	UC; E4	Negative	Bloody diarrhea (7.0), diagnosed with pancolitis (7.1). Single episode of pancreatitis (13.3). In clinical remission since age 13.3	Focal cryptitis, crypt abscesses, moderate architectural distortion, Paneth cell metaplasia	5-ASA, SALZ, CS

Abbreviations: AB, oral or intravenous antibiotics given for treatment of colitis, bowel decontamination, and fistula treatment; ADA, adalimumab; 5-ASA, 5-aminosalicylic acid; AZA, azathioprine; CD, Crohn's disease; CS, corticosteroids; EBV, Epstein-Barr virus; EIMs, extra-intestinal manifestations; F, female; HLH, hemophagocytic lymphohistiocytosis; IBDU, IBD unclassified; IFX, infliximab; M, male; MTX, methotrexate; NUT, polymeric/elemental diet; PR, per rectum; SALZ, sulfasalazine; UC, ulcerative colitis.

*ex vivo* biopsies obtained from lower compared to the upper GI tract suggesting that NOX1 is the primary source of superoxide in the non-inflamed colonic epithelium (**Supplementary Figure S3b,c**).

We visualized superoxide production of colonic crypts *ex vivo* using nitroblue tetrazolium chloride. Reaction of nitroblue tetrazolium chloride with superoxide results in formation of water-insoluble blue formazan precipitates,



**Figure 1** Clinical phenotype of the NOX1 p.N122H patient and NOX1 contribution to baseline reactive oxygen species (ROS) within colonic crypts. **(a)** Endoscopy and histology from NOX1 mutant patient. Colonoscopy shows loss of vascular pattern, ulceration, and luminal bleeding (left). Hematoxylin and eosin stain of colonic biopsies shows crypt architectural distortion and dense inflammatory cell infiltrate in the lamina propria (scale bar = 50  $\mu$ m, middle). Magnification of NOX1 mutant epithelial crypt demonstrates elongated nuclei (black arrow head) and crypt abscesses (white arrow head, right). **(b)** Family pedigree and Sanger sequencing of *NOX1* gene around the mutation site in a wild-type control and family members. **(c)** NOX1 protein sequence alignment of different genera showing the evolutionary-conserved asparagine at position 122. **(d)** The NOX1 variant p.N122H affects all three isoforms of NOX1. Amino-acid sequence was aligned using ClustalW. **(e)** Analysis of *NOX1*, *NOXA1*, and *NOXO1* expression by quantitative PCR in biopsies of the gastrointestinal tract. Single biopsies per segment were obtained from four to seven non-inflamed individuals. Bars represent mean. Statistical significance was determined by Mann–Whitney *U*-test. **(f)** *Ex vivo* colonic biopsies (within 90 min of collection) were incubated with nitroblue tetrazolium (NBT) in phosphate-buffered saline-glucose at room temperature. Biopsy specimens were analyzed using light microscopy immediately after 60 min NBT incubation (top left, biopsy overview showing dark crypts containing reduced formazan; bottom, ring-like deposition of formazan at epithelial margin of crypts; top right, single colonic epithelial crypt captured longitudinally at high magnification). **(g)** Microscopy of ROS-producing epithelial cells in colonic crypts of *ex vivo* biopsies detected by NBT dye ( $\times 200$  magnification). After 60 min of incubation a ring-like deposition of formazan at the epithelial margin of crypts was evident. In indicated conditions biopsies were co-incubated with either a NOX1 inhibitor (ML171) or a non-specific NADPH oxidase inhibitor (diphenyleneiodonium; DPI), to verify the signal. **(h, left)** DPI or ML171 inhibit superoxide generation and L-012-enhanced chemiluminescence on colonic biopsy specimens *ex vivo*. Following the detection of superoxide at baseline, DPI, ML171, or vehicle were added (black arrow) and chemiluminescence was recorded over 60 min. For each biopsy light emission was normalized to baseline reading. Data represent mean of nine biopsies per condition obtained from five non-inflamed controls. **(h, right)** Results of kinetic assay calculated as area under the curve per patient. Statistical significance was determined by Mann–Whitney *U*-test.



which can be observed by light microscopy (**Figure 1f**). Following 60 min incubation, we observed the deposition of formazan at the outer margin of colonic crypts indicating the constitutive release of superoxide from the colonic epithelium into the crypt lumen (**Figure 1f**). Co-incubation with ML171 (ref. 24) or diphenyleiiodonium (DPI), both NADPH oxidase inhibitors, suggested a reduction of superoxide production (**Figure 1g**). This finding was confirmed by the luminescence assay (**Figure 1h**).

### **Ex vivo NOX1 biopsy and primary organoids**

To assess the functional consequences of p.N122H mutation on colonic epithelial ROS production, we first assessed superoxide release in *ex vivo* colonic biopsies from the index patient and compared those to biopsies from patients with IBD and non-inflamed controls. Although biopsies from the NOX1 p.N122H variant patient generated low level of superoxide, this was within the range seen in other patients with quiescent IBD and non-inflamed controls (**Figure 2a**). However, as phagocytes that express NOX2 are present in non-inflamed biopsies (**Supplementary Figure S3a**) and lamina propria infiltrating phagocytes likely contribute to ROS measurements in IBD patient biopsies, the assay specificity is limited and an epithelial NOX1 defect is potentially masked.

### **NOX1 p.N122H reduces ROS production in primary organoids**

To validate the functional impact of the genetic defect in epithelial cells, we generated primary epithelial organoids from colonic biopsy specimens of the NOX1 p.N122H patient, a male IBD control patient, and a healthy female control without IBD (**Figure 2b**). Both IBD patients were in clinical remission at the time of the endoscopy. Colonic organoids express NOX1 mRNA, along with its subunits NOXA1 and NOXO1, and this expression did not differ between the index p.N122H patient and the IBD control patient (**Figure 2c**). We found high DUOX2 mRNA expression but only minimal NOX2 expression in the colonic epithelial organoids reflecting the epithelial origin and the absence of phagocytes (**Supplementary Figure S3a**).

Colonic epithelial organoid cells carrying NOX1 p.N122H mutation produced significantly less constitutive superoxide than control organoid cells derived from the IBD patient or a patient without inflammatory disease (**Figure 2d**). Of note, whereas phorbol 12-myristate 13-acetate (PMA) stimulation increased superoxide generation by control organoids, PMA stimulation of NOX1 p.N122H organoids did not. Even after stimulation with PMA, superoxide production by NOX1 p.N122H organoids was significantly less than baseline ROS of IBD control organoids (**Figure 2d**).

### **Functional characterization of multiple NOX1 hemizygous variants in VEOIBD**

To find additional NOX1 variants in patients with VEOIBD we screened exomes of 1,878 pediatric IBD patients. We identified 5 additional non-synonymous variants in NOX1 in separate patients in whom no other known or plausible genetic monogenic diagnosis was established (**Table 1**). The missense variants were

predicted to be damaging by SIFT, PolyPhen-2, or CADD scores, and were rare (minor allele frequency <1%) genetic variants (**Supplementary Tables 1 and 2**). All variants changed conserved amino acids (**Supplementary Figure S4**) and were found in regions with significant homology between NOX1 and NOX2 (**Supplementary Figure S5**).

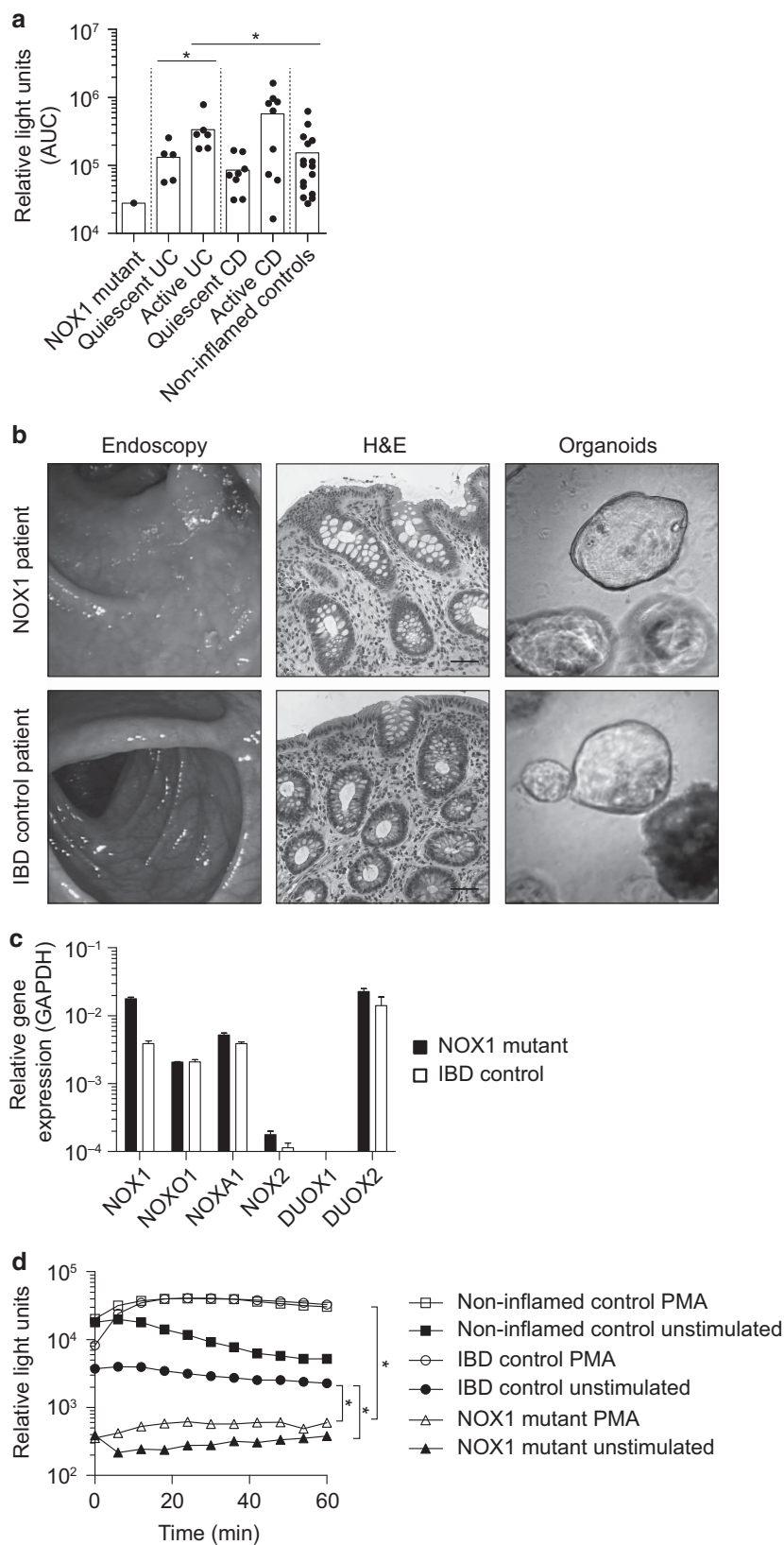
To characterize the functional impact of those variants we transfected the multimeric NADPH oxidase complex 1 in the colonic epithelial cell line HCT116. Alongside the rare NOX1 variants p.N122H, p.I67M, p.R287Q, p.Q293R, p.Y470H, and p.T497A that we identified in this study, we tested the previously described p.P330S variant<sup>13</sup> and the common polymorphism p.D360N (allele frequency European-non-Finnish, 2.4%). Three variants in patients P14, P15, and P16 affected potential splice sites, which we could not assess functionally (**Supplementary Tables 1, 2, and 4**). We used HCT116 cells as these cells express only low levels of NOX1 subunits (data not shown) and endogenous ROS generation cannot be detected (**Figure 3a**). Co-expression of wild-type NOX1 together with the subunits NOXA1 and NOXO1 resulted in superoxide generation in unstimulated and PMA-stimulated condition (**Figure 3a,b**). In contrast, co-expression with NOX1 variants variably diminished ROS generation. Whereas NOX1 variants p.N122H (index patient) and p.T497A completely abrogated both spontaneous and PMA-induced ROS production, the NOX1 variants p.I67M, p.R287Q, p.Q293R, p.P330S, p.D360N (common polymorphism), or p.Y470H were observed to either decrease spontaneous ROS and/or diminish PMA-stimulated ROS (**Figure 3a,b**). Expression levels of wild-type and variant NOX1 constructs were comparable (data not shown). This suggests that the rare genetic variants affected the ROS production to a variable degree between complete loss-of-function and moderate reduction comparable to polymorphisms.

### **Characteristics of patients with loss-of-function NOX1 variants**

We analyzed the IBD phenotype in all male patients with confirmed loss-of-function NOX1 variants (**Table 1** and **Supplementary Table 4**). Out of the 10 male patients with hemizygous NOX1 mutations, 4 presented with CD, 3 with UC, and 3 with IBD unclassified. In congruency with NOX1 expression, disease location was always colonic, with two patients also having perianal disease. Median age of onset was 7.9 years (range 1.8–10.5 years). Medical treatment included corticosteroids, aminosalicylates, azathioprine, methotrexate, or anti-tumor necrosis factor (infliximab or adalimumab in 4 of 8 patients) and 1 patient underwent ileocecal resection for stricture. No infections with intestinal pathogens were recorded. With exception of the index patient, no other severe hemophagocytic lymphohistiocytosis / Epstein–Barr virus-driven pathologies were recorded.

### **Population-based characteristics of genetic loss-of-function NOX1 variants**

In addition to those rare variants in NOX1, common polymorphisms might similarly contribute to IBD susceptibility. Of note, the common NOX1 polymorphism p.D360N has recently been associated with UC in Ashkenazi Jewish



**Figure 2** For caption see page 568.



males.<sup>13</sup> To determine whether this is Ashkenazi Jewish-specific or an association across several populations, we performed a genetic analysis of individuals of non-Jewish European ancestry. Although we observed a trend in the US European ancestry cohort (Table 2; Supplementary Tables 5 and 6), neither analysis of allele counts in UK cohorts nor analysis of summed allele counts from a total of 9,513 healthy controls and 11,140 IBD patients revealed an association (Table 2). This suggests that the association of NOX1 p.D360N with UC in males is not present across different populations. Variation is also reflected by a variable distribution of p.D360N allele frequency across populations (Figure 4a).

To further understand the importance of NOX1 variation, we compared the frequency of hemizygous NOX1 missense and NOX1 loss-of-function variants (STOP codon, frameshift, and predicted splice site), with those in NOX2, the causative gene of most patients with chronic granulomatous disease. The frequency of genetic missense variation in NOX1 is higher as compared to the homologous NOX2 (Figure 4b). Similarly, the constraint metric based on the ExAC data set indicates that loss-of-function variants in NOX1 are tolerated as indicated by a probability of being loss-of-function intolerant<sup>25</sup> of 0 (Figure 4c). In contrast NOX2 is extremely intolerant to any loss-of-function variation (probability of loss-of-function

intolerant 0.998)<sup>25</sup> as are many other genes causing X-linked primary immunodeficiencies (Figure 4c). This suggests that NOX1 underwent less evolutionary pressure as compared to NOX2 or other X-linked immunodeficiency genes.

Table 2 Population genetics of p.D360N variant

Gender	Ancestry	Group	N	MAF (%)	P-value, cases vs. controls	OR
Male	European	Control	4,744	2.66		
		IBD	5,549	2.74	0.843	1.03
		UC	2,462	3.45	0.068	1.31
		CD	2,895	2.18	0.217	0.82
	Ashkenazi Jewish <sup>13</sup>	Control	1,708	0.82		
		UC	297	3.37	1.25 × 10 <sup>-3</sup>	4.22
Female	European	Control	4,769	2.44		
		IBD	5,587	2.77	0.149	1.14
		UC	2,263	3.05	0.041	1.26
		CD	3,138	2.50	0.857	1.02
	Ashkenazi Jewish <sup>13</sup>	Control	906	0.99		
		UC	262	1.53	0.343	1.55

Abbreviations: CD, Crohn's disease; IBD, inflammatory bowel disease; MAF, minor allele frequency; OR, odds ratio; UC, ulcerative colitis. P-values were determined by the ALLELIC test or Fisher's exact method.<sup>13</sup>

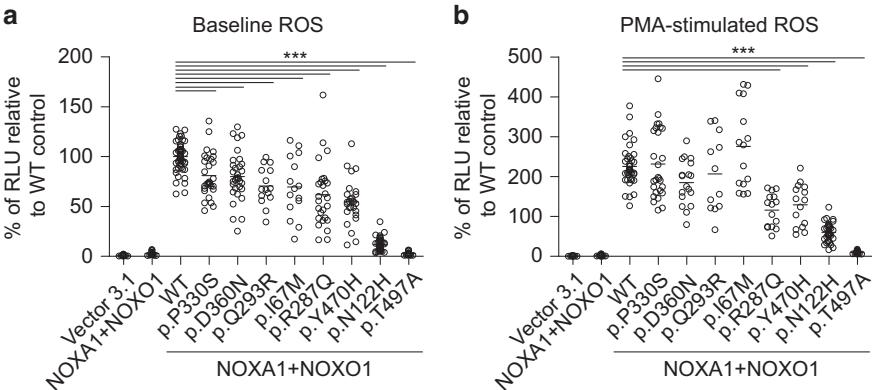
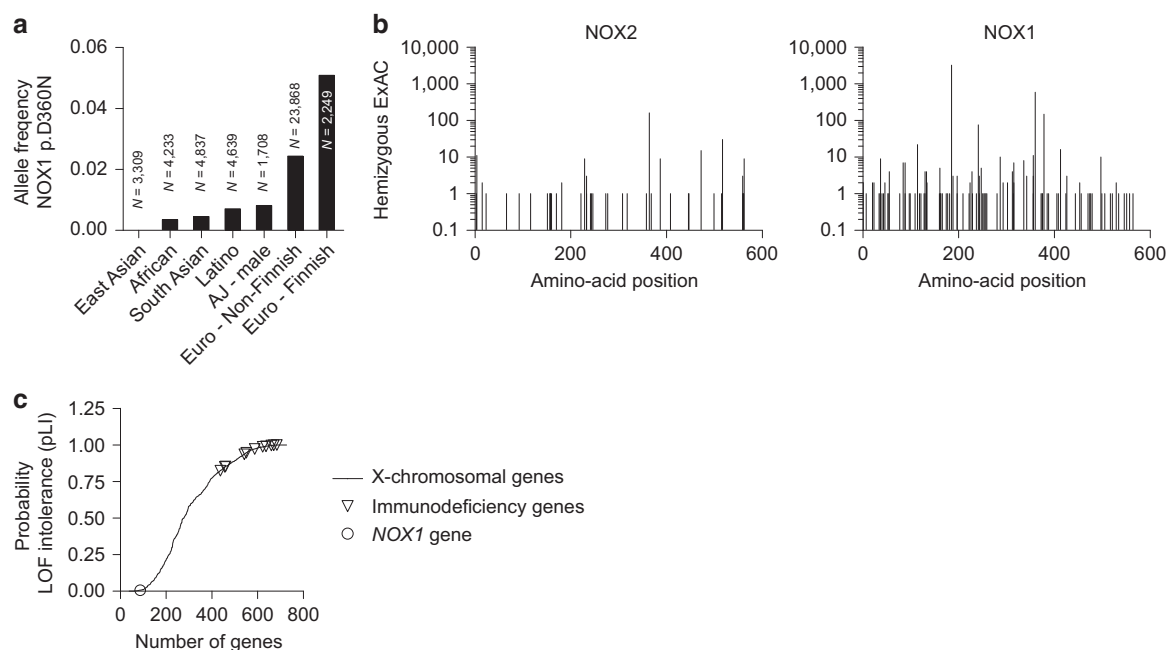


Figure 3 Comparative analysis of NOX1 variants. (a, b) Generation of superoxide in colonic epithelial cell line HCT116 reconstituted with multimeric NADPH oxidase complex and expressing wild-type or variant NOX1. ROS was analyzed by L-012-enhanced chemiluminescence in the absence (a) or presence of phorbol 12-myristate 13-acetate (PMA) (b). Chemiluminescence was measured 48 h post transfection and recorded over 60 min. Results represent eight independent experiments with 3–4 replicates. Each dot represents one replicate. Experiments were normalized to mean relative light units (RLUs) without PMA. Line represents mean. Statistical significance was determined with analysis of variance and post-test correction performed with Dunnett (multiple comparisons to one single control).

Figure 2 NOX1 p.N122H diminishes epithelial reactive oxygen species in primary organoids. (a) Superoxide generation of colonic epithelial biopsies measured over 60 min by L-012-enhanced chemiluminescence and total light emission quantified by area under the curve (AUC). Results are derived from 17 patients with colonic Crohn's disease (active disease  $n = 10$ ), 11 patients with ulcerative colitis (active disease  $n = 6$ ), 16 non-inflamed controls, and the patient with NOX1 p.N122H mutation. One symbol represents the mean of 1–3 pan-colonic biopsy specimens (both right- and left-sided) per patient. Active vs. quiescent disease dichotomized according to composite assessment, including endoscopic appearance (mucosal ulceration, loss of vascular pattern, and bleeding), biomarkers (C-reactive protein (CRP)), and histology (density of inflammatory infiltrate, cryptitis, and crypt abscesses). Statistical significance was determined by Mann–Whitney  $U$  test. (b) Organoids from patient with NOX1 mutation p.N122H and inflammatory bowel disease (IBD) control patient were generated from colonic biopsies obtained during quiescent disease state. Representative images of endoscopy, histology (hematoxylin and eosin staining, scale bar = 50  $\mu$ m), and organoids are displayed. (c) Analysis of NADPH oxidases and certain subunits by quantitative PCR in NOX1 p.N122H patient and IBD control organoids. (d) Kinetic assay of phorbol 12-myristate 13-acetate (PMA)-activated L-012-enhanced chemiluminescence on NOX1 p.N122H mutant, IBD control, and non-inflamed control organoid cells. Relative light units were measured over 60 min. Results are representative of two independent experiments measured in replicates. Statistical significance was determined by Wilcoxon signed-rank test comparing the AUC.



**Figure 4** NOX1 population frequencies and genetic variation. **(a)** Allele frequency of NOX1 p.D360N in different populations according to Exome Aggregation Consortium (ExAC) data and published literature.<sup>13</sup> **(b)** Number of hemizygotes found for a given variant (missense, nonsense, and frameshift) in NOX2 and NOX1 is plotted according to amino-acid position (x-axis). Frequency is based on ExAC data. **(c)** Probability of loss-of-function intolerance (pLI) of 727 human X-chromosomal genes based on ExAC data. X-linked primary immunodeficiency genes and NOX1 gene are highlighted.

In summary, our data suggest that NOX1 is the key NADPH oxidase for baseline ROS in human colonic crypt epithelium. Complete loss-of-function variants in NOX1 are rare and not associated with a distinct IBD sub-phenotype. Population statistics suggest that loss-of-function variants in NOX1 are rare but likely tolerated.

## DISCUSSION

In this study we investigated rare X-linked variants in NOX1 in eight male IBD patients. Functional analysis suggests a variant-dependent loss of NOX1-mediated superoxide generation. The clinical phenotype of affected patients was early onset of IBD with progressive and severe colonic disease, refractory to conventional therapy. The affected cohort demonstrates that NOX1-dependent ROS production is essential for superoxide production in colonic crypts.

Our characterization of six rare variants in NOX1 (p.I67M, p.N122H, p.R287Q, p.Q293R, p.Y470H, and p.T497A) expands the recent description of the rare NOX1 variant p.P330S and the common NOX1 polymorphism p.D360N in two male VEOIBD patients.<sup>13</sup> Furthermore, the NOX1 variant p.R287Q, which is functionally characterized in this study, has also been described but not characterized in an independent cohort of children with VEOIBD, adding further weight to the significance of epithelial NOX1.<sup>26</sup>

Diverse mechanisms maintain intestinal epithelial integrity, which serves as a critical barrier to luminal bacteria, viruses, and fungi.<sup>1,2</sup> Amongst these, NOX1 is likely to have a relevant role.<sup>27,28</sup> The generation of superoxide by NOX1 at the colonic epithelial border may have an anti-adhesive or anti-invasive effect on bacteria, contributing to the barrier function of the

inner mucus layer within colonic crypts. Indeed, our data confirm previous findings that the gene expression of NOX1 follows the density of bacterial colonization in the GI tract.<sup>17–20</sup> Reduced generation of superoxide due to genetic variants in NOX1 may affect crypt homeostasis allowing subsequent crypt colonization by luminal microbiota. NOX1-derived superoxide also influences intestinal epithelial differentiation and goblet cell function.<sup>29–31</sup> Colonic mucus produced by goblet cells provides an important barrier between the intestinal microbiota and the colonic epithelium, maintaining sterility at the epithelial border.<sup>32</sup>

The importance of NADPH oxidases for barrier function is also exemplified by DUOX2, an NADPH oxidase family member, which is expressed throughout the GI tract. Notably, defects in DUOX2 have been recently described as a potential susceptibility factor in patients with VEOIBD.<sup>13,33</sup> In animal models, defects in the *Drosophila duox2* homolog or in Zebrafish increased susceptibility against enteropathogens.<sup>34,35</sup> Whereas Duoxa<sup>−/−</sup> mice on thyroid hormone replacement showed normal growth and no evident phenotype,<sup>36</sup> recent studies suggested that colonization of segmented filamentous bacteria in the ileum, bacterial translocation into mesenteric lymph nodes, and *Salmonella typhimurium* systemic dissemination, is dependent on DUOX activity.<sup>37</sup> Although DUOX2 expression is inducible and is increased in patients with intestinal inflammation<sup>33,38</sup> thereby potentially contributing to epithelial stress and intestinal tissue damage, these data indicate that DUOX activity may be a functional mechanism that restricts bacterial colonization at the mucosal interface.

Interestingly, NOX1 activity regulates DUOX2 expression in the intestinal epithelium during *Citrobacter rodentium*

infection.<sup>39</sup> Although loss of epithelial *Cyba* protected against *C. rodentium* and *Listeria monocytogenes* infection, this is likely an indirect effect due to the resulting overgrowth of H<sub>2</sub>O<sub>2</sub>-producing lactobacilli.<sup>39</sup> This suggests an unexpected level of functional hierarchy and complex collaboration between NOX1 and DUOX2.<sup>39</sup>

Despite the complete loss of brush border ROS that has been observed in two NOX1 variants (p.N122H and p.T497A), we have not observed an increased susceptibility to intestinal infections such as *Salmonella* or *Yersinia*. This is in agreement with recent data suggesting that lack of Nox1 does not affect infection susceptibility in a mouse model of *Salmonella typhimurium*-induced typhlitis.<sup>40</sup> Nonetheless, larger patient numbers with complete loss-of-function NOX1 variants are required to more definitively determine the impact of these mutations on susceptibility to infection. Interestingly, the patient with the p.N122H mutation developed severe hemophagocytic lymphohistiocytosis in the context of Epstein–Barr virus infection whilst on azathioprine therapy.<sup>41</sup> Viral spreading has been shown to be increased in Nox1-deficient mice infected with influenza virus,<sup>42</sup> implicating a role for NOX1 in viral control. Again, larger patient numbers are required to fully understand the penetrance of the NOX1 variant phenotype.

Given the relatively high load of non-synonymous mutations of NOX1 compared to NOX2 and the large number of DUOX2 mutations in humans, it is likely that NOX/DUOX enzymes have partially redundant functions. It is therefore likely that both NOX1 and DUOX2 have a role in susceptibility to intestinal inflammation, and loss-of-function variants alone cause not highly penetrant Mendelian-type disorders. In keeping with a second hit hypothesis, Nox1 deficiency in interleukin-10-deficient mice resulted in earlier and more severe intestinal pathology, but loss of Nox1 alone did not cause intestinal inflammation.<sup>30</sup> Similarly, patients with congenital secretory diarrhea due to activating mutations in the guanylate cyclase C (GC-C)<sup>7,43</sup> or inactivating mutations in *SLC9A3* encoding for the sodium/proton exchanger NHE3,<sup>8</sup> a downstream target of GC-C, may also present with an IBD phenotype. In these patients the decreased epithelial uptake of sodium results in changes of mucosal ion content and pH, and Nhe3 deficiency in mice leads to an altered composition of the intestinal microbiota.<sup>44,45</sup> This dysbiosis drives intestinal inflammation in a T-cell-dependent model of intestinal inflammation.<sup>46</sup> Our studies suggest that loss of ROS at the colonic crypt may have a similar effect on barrier function.

Altogether these data suggest a highly context specific role of epithelial NADPH oxidases in intestinal homeostasis. Whilst in some animal models, a lack of interleukin-10 and Nox1 increases epithelial stress and susceptibility to colitis,<sup>30</sup> in other instances, lack of NADPH oxidase activity is protective. Indeed a protective role of Nox1 and Duox2 is suggested in a mouse model of ileocolitis caused by lack of protective glutathione peroxidase factors.<sup>47–49</sup> In this model GPx1- and GPx2-knockout leads to oxidative stress caused by Nox1 and Duox2 with a dominant role of Nox1 for crypt epithelial apoptosis.<sup>48,49</sup> This oxidative stress is dependent on the presence of the

intestinal microbiota as germ-free mice are protected and colitis develops within 1 week of bacterial colonization.<sup>50</sup> Given the role of NOX1 as a modifier of intestinal microbiota, we can only speculate whether IBD patients with loss-of-function NOX1 variants would benefit from therapeutic microbiome-altering strategies (e.g., antibiotics, nutrition, probiotics, or fecal transplant). Further studies characterizing the human gut microbiota in the setting of NOX1 deficiency are required.

It is possible that the human population genetics reflect this context specific role of NOX1. Whereas in populations like Ashkenazi Jews, the hemizygous NOX1 p.D360N variant is associated with UC, in European descent populations it is not. Substantially stronger genetic variation of NOX1 compared to NOX2 suggests that the overall impact on disease susceptibility of these genes is significantly different despite the high degree of protein conservation and similarity. It is even possible that the degree of genetic variation in NOX1 is caused by environmental factors such as infections where reduced ROS is protective.

In conclusion, we report six novel variants in the NOX1 gene in patients with IBD, two of which are associated with complete loss of function of the gene product and with loss of ROS production. Our study illustrates the complexity of epithelial barrier function in the pathogenesis of IBD and the need better to understand the functional impact of ROS production at the colonic crypt epithelium as a cause of colonic inflammation.

## METHODS

**Human subjects.** The recruitment of participants was approved by relevant ethics committees or institutional review boards at the individual contributing institution. Written informed consent was obtained from all patients/legal guardians and healthy controls.

Patients with IBD (including the index patient P1) and controls without intestinal inflammation were prospectively recruited as a part of the Oxford IBD cohort study or the Oxford Gastrointestinal Illness Biobank (REC 09/H1204/30 and REC 11/YH/0020). Replication genotyping of the p.N122H variant was performed in 2,767 IBD patients and 1,862 non-IBD controls. These individuals were enrolled by the UK IBD Genetics Consortium (<http://www.ibdresearch.co.uk/>). Exomes of 1,878 pediatric-onset IBD patients without genetic diagnosis were screened for additional rare NOX1 variants. Samples were previously genotyped as part of the COLORS in IBD study ( $n = 150$ ; Oxford, UK), the NEOPICS consortium ( $n = 545$ ; Toronto, ON, Canada; [www.neopics.org](http://www.neopics.org)), or the RISK cohort<sup>51</sup> ( $n = 1,183$ ; Atlanta, GA, USA). Genetic association testing of NOX1 p.D360N (rs34688635) was conducted on genotype data from IBD patients of non-Jewish European ancestry from the following cohorts: the European ancestry exome chip data set<sup>52</sup> ( $n = 10,523$ ); the Oxford IBD cohort study ( $n = 513$ ); and the COLORS in IBD study ( $n = 104$ ). Sequence data from healthy individuals were obtained from the European ancestry exome chip data set<sup>52</sup> ( $n = 5,726$ ) and the INTERVAL study ( $n = 4,436$ ; [www.intervalstudy.org.uk](http://www.intervalstudy.org.uk)). Population controls were also obtained from the UK10K project ([www.uk10k.org](http://www.uk10k.org)).

## Genotyping

**Whole-genome sequencing and NOX1 variant p.N122H identification.** The index mutation in NOX1 was identified by whole-genome sequencing as part of the WGS500 project.<sup>53</sup> DNA was analyzed from peripheral blood mononuclear cells. In summary, whole-genome sequencing was performed on 3.5–7.5 ng DNA on either the Illumina HiSeq2000 (Cambridge, UK) or the HiSeq2500 run in standard mode using v2.5 or v3 sequencing chemistry. The genomic DNA was fragmented, end-paired, A-tailed, and adapter-ligated before size



selection and amplification for a multiplexed library preparation as described in Taylor *et al.*<sup>53</sup> The libraries were paired-end sequenced and sequenced to an average coverage between 27 and 40 quality reads per base. Resulting 100 base pair reads were mapped to the GRCh37d5/hg19 human reference sequence using Stampy and the single-nucleotide variants and short InDels were called with Platypus.<sup>54</sup> Variant files were analyzed using Qiagen's Ingenuity Variant Analysis software (www.qiagen.com/Ingenuity; Qiagen Redwood City, CA, USA). High-quality calls were analyzed. For candidate analysis, we investigated a gene list of known variants associated with monogenic forms of IBD.<sup>5</sup> Filters for variant frequency (<1%; 1000 Genomes Project) and predicted deleterious filters (SIFT and PolyPhen) were applied to prioritize high quality calls for non-synonymous and likely pathogenic variants.

**Replication genotyping of the p.N122H variant.** Replication genotyping on the Sequenom plex was carried out at the Sanger Institute.

**Whole-exome sequencing.** Regeneron performed whole-exome sequencing on a cohort of 1,183 probands with pediatric-onset IBD (ages 0–18.5 years), including their affected and unaffected parents and siblings, where available (total samples = 2,704). Sample preparation, whole-exome sequencing, and sequence data production were performed as previously described.<sup>55</sup> The exomes of RISK cohort study participants (*n* = 545) were captured using SureSelect Human All Exon kit v2 (Agilent Technologies, Oxford, UK), using 3 µg of genomic DNA. Subsequently, captured libraries were sequenced on Illumina HiSeq2000 by 100-base pair paired-end sequencing. Image processing and base calling was performed using standard Illumina software. Raw sequence reads were mapped relative to the human genome reference sequence (GRCh38/hg38) using the PEMapper software tool (Cutler DJ *et al.*, submitted) to identify single-nucleotide variants.

**Sanger sequencing.** *NOX1* variants were validated using Sanger sequencing according to the standard techniques.

**Histology.** Historic routine hematoxylin and eosin histology sections from the patient identified to harbor the *NOX1* p.N122H mutation and IBD controls were analyzed. Staining of goblet cells or the proliferation marker Ki67 was performed on archived paraffin-embedded colonic epithelial biopsies. Specimens were stained using an Alcian blue and periodic acid-Schiff's reagent staining kit (Clin-Tech Limited, Guildford, UK) or rabbit monoclonal antibody to Ki67 (clone SP66, AbCam, Cambridge, USA), respectively. Nuclear fast red and hematoxylin (Sigma-Aldrich, Gillingham, UK) were used to counterstain cell nuclei.

**Protein sequence alignment.** Multiple sequences were aligned using ClustalW2.<sup>56</sup> Data were obtained from the National Center for Biotechnology Information. Sequence alignment is based on the following accession numbers: *Danio rerio*, NP\_001095857.1; *Xenopus tropicalis*, XP\_002939249.2; *Gallus gallus*, NP\_001095300.1; *Mus musculus*, NP\_757340.1; *Homo sapiens*, *NOX1* isoform 1–3, NP\_008983.2, NP\_039249.1, and NP\_001258744.1; *Homo sapiens*, *NOX2*, NP\_000388.2.

**Expression analysis.** Colonic biopsies were stored in RNAlater (Qiagen) before analysis. RNA was extracted using RNeasy kit (Qiagen), transcribed in cDNA with High Capacity cDNA Reverse Transcription Kit (Applied Biosystems, Waltham, MA), and expression data were obtained using TaqMan primers (Life Technologies, Paisley, UK) for *NOX 1-5*, *NOXO1*, *NOXA1*, *DUOX1*, and *DUOX2*. Results were normalized to *GAPDH* expression. Relative gene expression was calculated using the  $\Delta\Delta C_t$  method.

**Colonic epithelial organoid cultures.** Human colon crypts were isolated and organoids were cultured as previously described.<sup>57</sup> Briefly, crypts were embedded in Cultrex Reduced Growth Factor Basement Membrane Extract, Type 2 RGF PathClear (Amsbio, Abingdon, UK) and seeded in 48-well plates. The Basement Membrane Extract was

polymerized for 10 min at 37 °C, and 250 µl per well of organoid culture media was added. Organoid culture media consisted of advanced Dulbecco's modified eagle medium/F12 supplemented with penicillin/streptomycin (10 mmol l<sup>-1</sup>), HEPES (1 M), Glutamax (10 mmol l<sup>-1</sup>), and the following growth factors: Wnt conditioned media (50%) B27 (1 ×), epidermal growth factor (50 ng ml<sup>-1</sup>), Noggin (10%), R spondin (20%), gastrin (10 nM), nicotinamide (10 mM), A83-01 (500 nM), and SB202190 (10 µM). Y-27632 (10 µmol l<sup>-1</sup>; Sigma) was included in the medium for the first 5 days in culture. Once organoid growth was established, the culture media was refreshed every 3 days.

**Transfection of HCT116 cells.** The colonic epithelial cell line HCT116 was maintained in McCoy's 5A Modified (Gibco, Paisley, UK) supplemented with 10% fetal bovine serum. Cell systems were based on reconstitution of the multimeric *NOX1* complex containing *NOX1*, *NOXO1*, and *NOXA1* in HCT116 cells. pcDNA3.1-hNox1, pcDNA3.1-hNoxa1, and pcDNA3.1-hNoxo1 were kind gifts from Botond Banfi & Karl-Heinz Krause (Addgene, Cambridge, MA, plasmid # 58344, # 58531, and # 58530).<sup>19,58</sup> Mutations were introduced using site-directed mutagenesis and were verified by sequencing (Eurofins Genomics, Ebersberg, Germany). HCT116 cells were transfected with Lipofectamine 2000 (Invitrogen, Paisley, UK) following the manufacturer's instructions. Expression of wild-type and *NOX1* variants was confirmed by quantitative PCR. ROS production was analyzed by L-012-enhanced chemiluminescence 48 h post transfection.

**ROS assays.** ROS generation by colonic epithelial biopsies, organoid cells, and transiently transfected HCT116 cells was measured using L-012-enhanced chemiluminescence (Wako Laboratories, Neuss, Germany). After washing with phosphate-buffered saline, cells or biopsies were pre-incubated in L-012 (100 µM) for 10 min, followed by stimulation with PMA (5 µg ml<sup>-1</sup>, Sigma) or addition of diphenyleneiodonium (DPI, 10 µM, Sigma) and 2-acetylphenothiazine (ML171, 10 µM, Tocris, Bristol, UK) in indicated conditions. Emission of light was recorded at baseline and thereafter as a kinetic assay every 1–10 min in opaque white 96-well plates (FLUOstar OPTIMA, BMG Labtech, Aylesbury, UK).

For standardization, all intestinal epithelial biopsies were collected using Olympus (Southend-on-Sea, UK). EndoJaw needle forceps with a cup-opening size of 7.2 mm and analyzed within 90 min of collection with minimal handling. Organoids were trypsinized into single-cell suspension using TrypLETM express (Gibco), counted, and equal cell numbers dispensed into white 96-well plates.

For microscopy of ROS-producing epithelial cells, *ex vivo* colonic biopsies were incubated with 100 µg ml<sup>-1</sup> nitroblue tetrazolium chloride (Sigma) in phosphate-buffered saline-glucose (1 g l<sup>-1</sup>) with or without NADPH oxidase inhibitors. After 60 min incubation, formation of formazan was analyzed by light microscopy (Carl Zeiss Axioskop2, Cambridge, UK, × 200 magnification) on glass slides without coverslips. Images were photographed using Q-Imaging software (Surrey, BC, Canada). Microscopy images were cropped and analyzed using ImageJ software.<sup>59</sup>

Disease activity amongst IBD patients was characterized as active or quiescent on the basis of clinical symptoms (diarrhea, rectal bleeding, and abdominal pain), endoscopic features (mucosal vascular pattern, bleeding, or ulceration), histological features (cryptitis and crypt abscesses, and lamina propria polymorphonuclear cell infiltrate), and serum biomarkers (C-reactive protein).

**Data and statistical analysis.** All the data analyses were performed using GraphPad Prism version 5.02 (GraphPad Software, San Diego, CA) or R (The Foundation for Statistical Computing, R version 3.2.2, Vienna, Austria). Unpaired data were compared using Mann-Whitney *U*-test and paired data were compared with Wilcoxon signed-rank test. Significance of differences between multiple groups was performed with analysis of variance and post-test correction with Dunnett. Genetic association testing in cases and controls was

conducted with the ALLELIC test.<sup>60</sup> Pooled analyses were performed on the summed allele counts of different cohorts. *P*-values of <0.05 after correction for multiple testing were considered significant.

**SUPPLEMENTARY MATERIAL** is linked to the online version of the paper at <http://www.nature.com/mi>

## ACKNOWLEDGMENTS

We thank all our patients and their families for participation in this study. We thank all contributors of the Oxford IBD cohort study in particular Carolina Arancibia and Sophia Bennett for help with Sanger sequencing.

Participants in the INTERVAL randomized controlled trial were recruited with the active collaboration of NHS Blood and Transplant England ([www.nhsbt.nhs.uk](http://www.nhsbt.nhs.uk)), which has supported field work and other elements of the trial. DNA extraction and genotyping was funded by the National Institute of Health Research (NIHR), the NIHR BioResource (<http://bioresearch.nihr.ac.uk/>), and the NIHR Cambridge Biomedical Research Centre ([www.cambridge-brc.org.uk](http://www.cambridge-brc.org.uk)). The academic coordinating centre for INTERVAL was supported by core funding from the following: NIHR Blood and Transplant Research Unit in Donor Health and Genomics; UK Medical Research Council (G0800270); British Heart Foundation (SP/09/002); and NIHR Research Cambridge Biomedical Research Centre. A complete list of the investigators and contributors to the INTERVAL trial is provided in reference.<sup>61</sup>

R.V.B. and H.H.U. were supported by the Medical Research Fund Oxford. Part of this work has formed the MScR thesis of R.V.B. T.S. is supported by the Deutsche Forschungsgemeinschaft (SCHW1730/1-1). H.H.U. and F.P. are supported by the Crohn's & Colitis Foundation of America (CCFA); A.M.M., H.H.U., D.P.B.M., and F.P. by The Leona M. and Harry B. Helmsley Charitable Trust; and H.H.U. by Crohn's and Colitis UK—for Crohn's—; H.H.U. and D.C.W. by ESPGHAN. S.P. was supported by a Boehringer Ingelheim Foundation grant. F.P. is supported by the Wellcome Trust. U.G.K. is supported by Science Foundation Ireland. The WGS500 Project was funded in part by Illumina. The Oxford IBD cohort is supported by Oxford BRC. L.M. and V.S.W.L. are supported by the Francis Crick Institute, which receives its core funding from Cancer Research UK, the UK Medical Research Council, and the Wellcome Trust. S.K. and L.D. are supported by R01 DK098231. R.K.R. is supported by a NHS Research Scotland Senior Fellowship. D.C.W. is supported by Medical Research Council and Medical Research Foundation for PICTS; Crohn's and Colitis UK. J.R.K. is supported by the National Institutes of Health (K23DK100461-01A1). D.P.B.M. is supported by P01 DK046763 and DK062413. This work was funded by a Wellcome Trust Core Award (090532/Z/09/Z) and a Medical Research Council Hub grant (G0900747 91070) to Peter Donnelly, the NIHR Biomedical Research Centre Oxford, the UK Department of Health's NIHR Biomedical Research Centres funding scheme, and Illumina. D.J.M. was supported by the General Sir John Monash Foundation, Australia.

## Web Resources

The URLs for data presented herein are as follows:

Plasmids, <https://www.addgene.org/>  
1000 Genomes, <http://browser.1000genomes.org>  
dbSNP, <http://www.ncbi.nlm.nih.gov/projects/SNP/>  
ExAC Browser, <http://exac.broadinstitute.org/>  
NHLBI Exome Sequencing Project (ESP) Exome Variant Server, <http://evs.gs.washington.edu/EVS/>  
OMIM, <http://www.omim.org/>  
HGMD, <http://www.hgmd.cf.ac.uk/ac/index.php>  
RefSeq, <http://www.ncbi.nlm.nih.gov/RefSeq>  
SIFT, <http://sift.jcvi.org/>  
PolyPhen-2, <http://genetics.bwh.harvard.edu/pph2/>  
PROVEAN, <http://provean.jcvi.org/index.php>  
Combined Annotation Dependent Depletion (CADD), <http://cadd.gs.washington.edu/>

## AUTHOR CONTRIBUTIONS

T.S., R.V.B., S.P., M.C., L.M., J.J., V.S.W.L., and H.H.U. designed and performed experiments, evaluated and interpreted data. K.M., K.F., P.B.S., A.R., S.P.L.T., R.K.R., D.C.W., J.R.K., L.A.D., S.K., A.M.M., R.H.D.,

D.P.B.M., C.G.M., J.S., W.H.O., D.J.R., J.D., and J.C. contributed patients, collected clinical data and samples, or screened cohorts. J.-B. C., M.P., C.G.M., R.C., E.G.S., C.A.A., R.H.D., D.P.B.M., and J.C. conducted bioinformatics and statistical analyses. U.G.K., F.P., V.S.W.L., A.M.M., E.G.S., C.A.A., R.H.D., D.P.B.M., D.J.M., and J.C. gave conceptual advice. H.H.U. drafted the manuscript and directed the study. All authors reviewed and contributed to the writing of the manuscript.

## DISCLOSURE

H.H.U. declares industrial project collaboration with Eli Lilly and UCB Pharma. Travel support was received from GSK foundation, Actelion, and MSD. T.S. received speaker's fees from MSD and travel support from Nestlé Nutrition. R.V.B. has received conference travel support from Janssen. R.V.B. has received speaker's fees from Janssen, Takeda, and Shire, and travel support from Takeda. S.P.L.T. has received Grants/Research Support from AbbVie, IOIBD, Lilly, UCB, Vifor, and Norman Collison Foundation; Consulting Fees and or travel support from AbbVie, Amgen, Asahi, Biogen, Boehringer Ingelheim, Bristol-Myers Squibb, Celgene, Chemocentryx, Cosmo, Ferring, Giuliani SpA, GlaxoSmithKline, Janssen, Lilly, MSD, Neovacs, NovoNordisk, Norman Collison Foundation, Novartis, NPS Pharmaceuticals, Pfizer, Proximagen, Receptos, Shire, Sigmoid Pharma, Takeda, Topivert, UCB, VHSquared, and Vifor; and Speaker fees from AbbVie, Amgen, Biogen, Ferring, and Takeda. R.K.R. has received speaker's fees, travel support, and participated in medical board meetings with MSD Immunology, Abbvie, Nestle, and Takeda. D.C.W. received investigator-initiated research funding from MSD, speaker's fees and travel support from AbbVie, and consultancy fee from Pfizer.

## WGS500 CONSORTIUM: NAMES AND AFFILIATIONS OF AUTHORS

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### Data Analysis

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